All Following Commands Entered into Mothur Software:

make.file(inputdir = . , type=fastq,prefix=stability)

make.contigs(file=stability.files, processors = 20)

summary.seqs(fasta= summary.trim.contigs.fasta)

screen.seqs(fasta=stability.trim.contigs.fasta, group = stability.contigs.groups, summary=stability.trim.contigs.summary, maxambig =0, maxlength=275)

unique.seqs(fasta = stability.trim.contigs.good.fasta)

count.seqs(name=stability.trim.contigs.good.names, group=stability.contigs.good.groups,processors=20)

summary.seqs(fasta=stability.trim.contigs.good.unique.fasta, count=stability.trim.contigs.good.count\_table)

align.seqs(fasta=stability.trim.contigs.good.unqiue.fasta, reference = silva.v4.fasta)

summary.seqs(fasta=stability.trim.contigs.good.unique.align, count=stability.trim.contigs.good.count\_table)

screen.seqs(fasts=stability.trim.contigs.good.unique.align, count=stability.trim.contigs.good.count\_table, summary=stability.trim.contigs.good.unique.summary, start=1968, end=11550)

summary.seqs(fasta=stability.trim.contigs.good.unique.good.align, count= stability.trim.contigs.good.good.count\_table)

filter.seqs(fasta=stability.trim.contigs.good.unique.good.align, vertical=T, trump=.)

unique.seqs(fasta=stability.trim.contigs.good.unique.good.filter.fasta, count = stability.trim.contigs.good.good.count\_table)

pre.cluster(fasta=stability.trim.contigs.good.unique.good.filter.unique.fasta, count= stability.trim.contigs.good.unique.good.filter.count\_table, diffs=2, processors=20)

chimera.vsearch(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta, count= stability.trim.contigs.good.unique.good.filter.unique.precluster.count\_table, dereplicate=t)

remove.seqs(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta, accnos=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.accnos)

summary.seqs(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.fasta, count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearh.pick.count\_table)

classify.seqs(fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.fasta, count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.count\_table, reference=trainset16\_022016.rdp.fasta, taxonomy=trainset16\_022016.rdp.tax, cutoff=80)

remove.lineage(fasta= stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.fasta, count= stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.count\_table, taxonomy=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.rdp.wang.taxonomy, taxon=Chloroplast-Mitochondria-unknown-Archaea-Eukaryota)

get.groups(count= stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.count\_table, fasta= stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.fasta, groups=Mock\_S280)

seq.error(fasta= stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.fasta, count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table, reference=HMP\_MOCK.v35.fasta, aligned=F)

dist.seqs(fasta= stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.fasta, cutoff=0.03)

cluster(column=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.dist, count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table)

make.shared(list=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.list, count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table, label=0.03)

rarefaction.single(shared=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.shared)

remove.groups(count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.count\_table, fasta=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.fasta, taxonomy= stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.rdp.wang.pick.taxonomy, groups=Mock\_S280)

cluster.split(fasta= stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.fasta, count= stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table, taxonomy= stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.rdp.wang.pick.pick.taxonomy, splitmethod=classify, taxlevel=4, cutoff=0.03)

make.shared(list=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.unique\_list.list, count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table, label=0.03)

classify.otu(list=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.unique\_list.list, count=stability.trim.contigs.good.unique.good.filter.unique.precluster.denovo.vsearch.pick.pick.pick.count\_table, taxonomy=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.rdp.wang.pick.pick.taxonomy, label=0.03)

rename.file(taxonomy=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.unique\_list.0.03.cons.taxonomy, shared=stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.pick.pick.opti\_mcc.unique\_list.shared)

count.groups(shared=stability.opti\_mcc.shared)

sub.sample(shared= stability.opti\_mcc.shared, size=2403)

rarefaction.single(shared= stability.opti\_mcc.shared, calc=sobs, freq=100)

summary.single(shared= stability.opti\_mcc.shared, calc=nseqs-coverage-sobs-invsimpson, subsample=T)

summary.single(shared= stability.opti\_mcc.shared, calc=nseqs-coverage-sobs-simpson, subsample=T)

summary.single(shared= stability.opti\_mcc.shared, calc=nseqs-coverage-sobs-chao, subsample=T)

summary.single(shared= stability.opti\_mcc.shared, calc=nseqs-coverage-sobs-ace, subsample=T)

summary.single(shared= stability.opti\_mcc.shared, calc=nseqs-coverage-sobs-shannon, subsample=T)

dist.seqs(shared= stability.opti\_mcc.shared, calc=thetayc-jclass, subsample=t)

pcoa(phylip= stability.opti\_mcc.thetayc.0.03.lt.ave.dist)

nmds(phylip= stability.opti\_mcc.thetayc.0.03.lt.ave.dist)

nmds(phylip= stability.opti\_mcc.thetayc.0.03.lt.ave.dist, mindim=3, maxdim=3)

amova(phylip= stability.opti\_mcc.thetayc.0.03.lt.ave.dist, design=Metadata.csv)

homova(phylip= stability.opti\_mcc.thetayc.0.03.lt.ave.dist, design=Metadata.csv)

corr.axes(axes=stability.opti\_mcc.thetayc.0.03.lt.ave.pcoa.axes, shared=stability.opti\_mcc.0.03.subsample.shared, method=spearman, numaxes=3)